

REMARKS

Status of the Claims

Claim 1 has been amended without prejudice to or disclaimer of the subject matter therein such that it now recites the following: "An isolated nucleic acid comprising a polynucleotide having at least 80% sequence identity to SEQ ID NO: 3, wherein said polynucleotide encodes a maize AFP1 protein, or a complement of said polynucleotide." Support for this amendment is found in original claim 1. New claims 13-17 have been added, drawn to the polynucleotide sequences of SEQ ID NOS:1, 3, 5, 7 and 9. Support for the new claims can be found in original claim 1. Therefore, no new matter has been added by amendment. Claims 1-17 are now pending.

With respect to Item 1 on the Office Action Summary, the Examiner has indicated that the Restriction Requirement is responsive to the Communication filed on February 5, 2003. Applicants wish to clarify that the Communication filed on February 5, 2003 was a Request for Corrected Filing Receipt.

It is not believed that extensions of time or fees for net addition of claims are required, beyond those that may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR § 1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-0605.

Respectfully submitted,



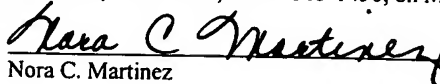
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CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on May 22, 2003.


Nora C. Martinez

Alignment of the Maize sequences:

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      1                               50
SEQ ID: 1 (1) ---ACCCACGCGTCCGCCACGCGTCCGC---AGCAATCCACACAAGCACT
SEQ ID: 3 (1) ---ACCCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 5 (1) TCGACCCAGCGCTCGGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 7 (1) TCGACCCAGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 9 (1) -----AGCG
Consensus (1) ACCCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      51                               100
1 (46) TCGAAGGACCACTG-CTCGGAG---GACACACCAAGCGTCTGCACCAAT
3 (48) TCGACGTACACGGGCGCTGCGCACAGACACACCAAGCGTCGGCACCAAT
5 (51) TCGACGTACACGGGCGCTGCGCACAGACACACCAAGCGTCGGCACCAAT
7 (51) TCGACGTACACGGGCGCTGCGCACAGACACACCAAGCGTCGGCACCAAT
9 (5) GCGGGGAAGAAGGGCTACAAGATGAAGACGACAGGGCGTCGGCACCAAT
Consensus (51) TCGACGTC CACGGGCGCTGCGCACAGACACCAAGCGTCGGCACCAAT

      101                               150
1 (91) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGG
3 (98) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGG
5 (101) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGG
7 (101) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGG
9 (55) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGG
Consensus (101) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGG

      151                               200
1 (141) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
3 (148) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
5 (151) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
7 (151) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
9 (105) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
Consensus (151) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC

      201                               250
1 (191) AAGGAGAAGTTCGAGGAGGTGACACGGTATCAGCGCCGGCGCCAAACCA
3 (198) AAGGAGAAGTTCGAGGAGGTGACACGGTATCAGCGCCGGCGCCAAACCA
5 (201) AAGGAGAAGTTCGAGGAGGTGACACGGTATCAGCGCCGGCGCCAAACCA
7 (201) AAGGAGAAGTTCGAGGAGGTGACACGGTATCAGCGCCGGCGCCAAACCA
9 (155) AAGGAGAAGTTCGAGGAGGTGACACGGTATCAGCGCCGGCGCCAAACCA
Consensus (201) AAGGAGAAGTTCGAGGAGGTGACACGGTATCAGCGCCGGCGCCAAACCA

      251                               300
1 (241) CCACCACCACCA---TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
3 (248) CCACCACCACCA---TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
5 (251) CCACCACCACCA---TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
7 (251) CCACCACCACCAATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
9 (205) CCACCACCACCA---TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
Consensus (251) CCACCACCACCA TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG

      301                               350
1 (288) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
3 (295) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
5 (298) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
7 (301) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
9 (252) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
Consensus (301) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG

      351                               400
1 (338) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG-CGGCCGG
3 (345) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG-CGGCCGG
5 (348) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG-CGGCCGG
7 (351) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG-CGGCCGG
9 (302) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCAECCCGGGCGGCCGG
Consensus (351) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG CGGCCGG

      401                               450
1 (387) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT
3 (394) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT
5 (397) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT
7 (400) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT
9 (352) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGATT
Consensus (401) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT

      451                               500
1 (437) GACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC
3 (444) GACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC
5 (447) GACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC
7 (450) GACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC

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9 (402) G--TG-----CAGGGTCATCGTACTTGGCTAGCGTACGTGCACGCACTC
Consensus (451) GACTGGTTGT CAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC
501 550
1 (487) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAACTTCT
3 (494) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAACTTCT
5 (497) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAACTTCT
7 (500) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAACTTCT
9 (444) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAACTTCT
Consensus (501) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAACTTCT
551 600
1 (537) TCGTAATACTAATACCTACATCAAAAAAAAAAAAAAAAAAAAAAAAAA
3 (544) TCGTAATACTAA-----AAAAAAAAAAAAAAAAAAAAAAAAA
5 (547) TCGTAATACTAA-----AAAAAAAAAAAAAAAAAAAAAAAAA
7 (550) TCGTAATACTAA-----AAAAAAAAAAAAAAAAAAAAAAAAA
9 (494) TCGTAATACTAATACCT-----AAAAAAAAAAAAAAAAAAAAAAAAA
Consensus (551) TCGTAATACTAA AAAAAAAAAAAAAAAAAAAAAAAAAA
601 650
1 (587) AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
3 (575) -----
5 (578) -----
7 (581) -----
9 (530) -----
Consensus (601) -----
651 690
1 (637) AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
3 (575) -----
5 (578) -----
7 (581) -----
9 (530) -----
Consensus (651) -----

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Maize Sequences: Gap-like results with Needleman-Wunsch algorithm

Seq1	Seq2	Overall id
3	1	82.1
3	5	99.48
3	7	86.76
3	9	86.76

Sequence #3's identity to the other sequences is shown above.

Pairwise Alignments of Sequence 3 versus each of the other maize sequences.
(Gap-like results with Needleman-Wunsch algorithm "Needle program")

GLOBAL: 3 VS 1
SCORE: 2683.50

3	1	ACCCACGCGTCCGCCCACGCGTCCGCACAGCAATCCACACAAGCA 45
1	1	ACCCACGCGTCCGCCCACGCGTCCG . CAGCAATCCACACAAGCA 43
3	46	CTTCGACGTCAACGGGCGCTGCGCACA . GACACACCAAGCGTCG 89
1	44	CTTCGA AGGACCACTGCTCGGAGGACACACCAAGCGTCT 82
3	90	GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAG 134
1	83	GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAG 127
3	135	GTGAGGTCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGCGGCGGC 179
1	128	GTGAGGTCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGCGGCGGC 172
3	180	GTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACG 224
1	173	GTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACG 217
3	225	GTCTCAGCGCCGGCGCCAACCACCACCACCACCATGGTCACCAC 269
1	218	GTATCAGCGCCGGCGCCAACCACCACCACCACCATGGTCACCAC 262
3	270	GGCGGCCACGGCTTCGTGGTGC GCGAGACCAGGGTCGAAGAGGAC 314
1	263	GGCGGCCACGGCTTCGTGGTGC GCGAGACCAGGGTCGAGGAGGAC 307
3	315	ATCAACACCTGCACCGCGAGGTCCACGAGCGCAGGGAGAGCTTC 359
1	308	ATCAACACCTGCACCGCGAGGTCCACGAGCGCAGGGAGAGCTTC 352
3	360	CTCGCCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGCC 404
1	353	CTCGCCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGCC 397
3	405	GTTCTGTCTTGCTGCTGCTTATGTATGTCTGTGGTTGACTGG 449
1	398	GTTCTGTCTTGCTGCTGCTTATGTATGTCTGTGGTTGACTGG 442
3	450	TTGTTTCAAGGTCATCGTACTTGGCTATCGTACGTGCACGCACTCA 494
1	443	TTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTCA 487
3	495	GCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAAC 539
1	488	GCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAAC 532
3	540	TTCTTCGTAATACTAA AAAAAAAAAAAAAAAAAAAAA 574
1	533	TTCTTCGTAATACTAATACTACATCAAAAAAAAAAAAAAAAAAAAA 577
3		
1	578	AA 622

3			
1	623	AA	667
3			
1	668	AAAAAAAAA	676
OVERALL %ID = 82.10		OVERALL %SIMILARITY = 82.10	

GLOBAL: 3 VS 5
SCORE: 2870.00

3	1	ACCCACGCGTCCGCCCACGCGTCCGCACAGCAATCCACACAA	42
5	1	TCGACCCACGCGTCCGCCCACGCGTCCGCACAGCAATCCACACAA	45
3	43	GCACTTCGACGTACACGGGCGCTGCGCACAGACACACCAAGCGT	87
5	46	GCACTTCGACGTACACGGGCGCTGCGCACAGACACACCAAGCGT	90
3	88	CGGCACCAATGGCTTACTACCAGGAGGTGGA	132
5	91	CGGCACCAATGGCTTACTACCAGGAGGTGGA	135
3	133	AGGTGAGGTGCGTGGCCCGGCGGCTTCGGCCGCCACGGCGGCG	177
5	136	AGGTGAGGTGCGTGGCCCGGCGGCTTCGGCCGCCACGGCGGCG	180
3	178	GCGTCCAGCAGCACGTGTCAGGAGAAGTTCGAGGAGGTGACA	222
5	181	GCGTCCAGCAGCACGTGTCAGGAGAAGTTCGAGGAGGTGACA	225
3	223	CGGTCTCAGCGCCGGCGCCAACCACCACCACCATGGTCACC	267
5	226	CGGTCTCAGCGCCGGCGCCAACCACCACCACCATGGTCACC	270
3	268	ACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGG	312
5	271	ACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGG	315
3	313	ACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCT	357
5	316	ACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCT	360
3	358	TCCTCGCCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGC	402
5	361	TCCTCGCCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGC	405
3	403	CCGTTGCTGCTGCGCTGCGTGCCTTATGTATGTCTGTGGTTGACT	447
5	406	CCGTTGCTGCTGCGCTGCGTGCCTTATGTATGTCTGTGGTTGACT	450
3	448	GGTTGTTTCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACT	492
5	451	GGTTGTTTCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACT	495
3	493	CAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAA	537
5	496	CAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAA	540
3	538	ACTTCTTCGTAATACTAAAAAAAAAAAAAAAAAAAAA	574
5	541	ACTTCTTCGTAATACTAAAAAAAAAAAAAAAAAAAAA	577

OVERALL %ID = 99.48

OVERALL %SIMILARITY = 99.48

SCORE: 2336.50

3 1 ACCCACGCGTCCGCCCACGCGTCCGCACAGCAATCCACACAAGCA 45

7 1 AG 2

3 46 CTTCGAC..GTCACACGGGC.....GCTGCGCACAGACACACCAA 83

7 3 ...CGGCGGGGAAGAAGGGCTACAAGATG...AAGACGCACAAG 40

3 84 GCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCG 128

7 41 GCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCG 85

3 129 GAGGAGGTGAGGTTCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGC 173

7 86 ||||| 130
GAGGAGGTGAGGTCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGC

3 174 GGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTC 218

7 131 GGCGGCGTCCAGCAGCACGTCGTCAGGAGAAAGTTCGAGGAGGTC 175

3 219 GACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACCATGGT 263

7
176 GACACGGTTCGCACGCGCGGGCGCCAACCAACCACCACCACCATGGT 220

3 264 CACCACGGCGGCCACGGCTTCGTGGTGC GCGAGACCAGGGTTCGAA 308

7
221
CACCACGGCGGCCACGGCTTCGTGGTGC GCGAGACCAGGGTTCGAG 265

3 309 GAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAG 353

7
266 GAGGACATCAACACCTGCACCGGCAGGTTCCACGAGCGCAGGGAG 311

3 354 AGCTTCCTCGCCAGGGCTAACTGAGCCGCCC GCGGGCCGGGCATC 387

7
311 AGCTTCCTGCCAGGGCTAACTGAGCAGCCCGGGCGGGCGGCATC 355

3 398 CACGCCCGTTCTGTGCTTGCCCTGCGTGCCCTTATGTATGTCTGTGCT 443

7 356 CACGCCCCGTTTCGTGCCTGCCTGCGTGCCTTATGTATGTCTG 396

3 443 TGA CTGGT TGTT CAGGGT CATCGT ACTTGGGCTATCGTACGTGCAC 487

7 397 TGAATGTTGTCAGGGTCATCGTACTTGGCTACGGTACGTGCAC 432

3 488 GCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTCAGCTCA 532

7 438 GCACCTACGCTCCTGTACGAATTACGATAATAAGCTCGTGAAGCTG 488

3 533 ATAAAACTTCTTCGTAATACTAA AAAAAAAAAAAAAAAAAA 572

5 355 ATAAAAATCTCTCGTAATACATA...AAAAAAAAAAAAAAAAAAAA 572
|||||

7 483 ATAAAACTTCTTCGTAAATACTAATACCTAAAAAAAAAAAAAAAAAAAA 522

3 573 AA 574

5	373	AA	574
7	528	AA	528

OVERALL %SIMILARITY = 86.76

OVERALL %SIMILARITY = 86.76

GLOBAL: 3 VS 9
SCORE: 2336.50

3	1	ACCCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCA	45
9	1		AG.. 2
3	46	CTTCGAC..GTCACACGGGC.....GCTGCGCACAGACACACCAA	83
9	3	...CGGCGGGGAAGAAGGGCTACAAGATG...AAGACGCACAAG	40
3	84	GCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCG	128
9	41	GCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCG	85
3	129	GAGGAGGTGAGGTGCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGC	173
9	86	GAGGAGGTGAGGTGCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGC	130
3	174	GGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTC	218
9	131	GGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTC	175
3	219	GACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACCATGGT	263
9	176	GACACGGTCGCACGCGCCGGCGCCAACCACCACCACCACCATGGT	220
3	264	CACCACGGCGGCCACGGCTTCGTGGTGCGGAGACCAGGGTCGAA	308
9	221	CACCACGGCGGCCACGGCTTCGTGGTGCGGAGACCAGGGTCGAG	265
3	309	GAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAG	353
9	266	GAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAG	310
3	354	AGCTTCCTCGCCAGGGCTAACTGAGCCGCCC.GGCGGCCGGCATC	397
9	311	AGCTTCCTCGCCAGGGCTAACTGAGCAGCCGGGCGGCCGGCATC	355
3	398	CACGCCCGTTTCGTGCTTGCCTGCGTGCCTTATGTATGTCTGTGGT	442
9	356	CACGCCCGTTTCGTGCTTGCCTGCGTGCCTTATGTATGTCTG... 396	
3	443	TGACTGGTTGTTACAGGTCATCGTACTTGGCTATCGTACGTGCAC	487
9	397	...TGATTGTGCAGGGTCATCGTACTTGGCTAGCGTACGTGCAC	437
3	488	GCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGA	532
9	438	GCACTCAGCTCCTGTACGAATTACGATAATAAGCTCGTGACCTGA	482
3	533	ATAAACTTCTTCGTAATACTAA...AAAAAAAAAAAAAAAAAA	572
9	483	ATAAACTTCTTCGTAATACTAATACCTAAAAAAAAAAAAAAAAAA	527
3	573	AA	574
9	528	AA	529

OVERALL %ID = 86.76

OVERALL %SIMILARITY = 86.76